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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: Thomsen *et al.*

Confirmation No. 8725

Application No.: 10/009,945

Art Unit: To Be Assigned

Filed: December 11, 2001

Examiner: To Be Assigned

For: ANTAGONISTS OF BMP AND TGF β
SIGNALING PATHWAYS

Atty Docket No.: 10624-092

TRANSMITTAL OF SEQUENCE LISTING

Assistant Commissioner for Patents
Washington, DC 20231

S I R :

In connection with the above-identified application, and in accordance with 37 C.F.R. § 1.821, Applicant submits herewith a Sequence Listing in paper and computer-readable format pursuant to 37 C.F.R. § 1.821(c) and (e).

I hereby state that the content of the paper and computer-readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same. I hereby state that the submission herein under 37 C.F.R. § 1.821(g) does not include new matter.

Respectfully submitted,

Date June 21, 2002

Anthony M. Insogna 35,203
Anthony M. Insogna (Reg. No.)

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Enclosures

by Eileen E. Fahy 46,077
(Reg. No.)



SEQUENCE LISTING

<110> The General
Wrana, Jeffery

<120> ANTAGONISTS OF BMP AND TGF-BETA SIGNALING PATHWAYS

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<170> PatentIn version 3.1

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Thr	Gln	Phe	Thr	Asp	Pro	Arg	Leu	His	His	Ile	Ile	Asn	His	Gln	Ser	
305					310					315					320	
Gln	Leu	Lys	Glu	Pro	Asn	His	Ala	Ile	Pro	Val	Gln	Ser	Asp	Gly	Ser	
				325					330					335		

Leu Glu Asp Gly Asp Glu Phe Pro Ala Gln Arg Tyr Glu Arg Asp Leu
 340 345 350
 Val Gln Lys Leu Lys Val Leu Arg His Glu Leu Ser Leu Leu Gln Pro
 355 360 365
 Gln Ala Gly His Cys Arg Val Glu Val Ser Arg Glu Glu Ile Phe Glu
 370 375 380
 Glu Ser Tyr Arg Gln Ile Met Lys Met Arg Pro Lys Asp Leu Lys Lys
 385 390 395 400
 Arg Leu Met Val Lys Phe Arg Gly Glu Glu Gly Leu Asp Tyr Gly Gly
 405 410 415
 Val Ala Arg Glu Trp Leu Tyr Leu Leu Cys His Glu Met Leu Asn Pro
 420 425 430
 Tyr Tyr Gly Leu Phe Gln Tyr Ser Thr Asp Asn Ile Tyr Thr Leu Gln
 435 440 445
 Ile Asn Pro Asp Ser Ser Ile Asn Pro Asp His Leu Ser Tyr Phe His
 450 455 460
 Phe Val Gly Arg Ile Met Gly Leu Ala Val Phe His Gly His Tyr Ile
 465 470 475 480
 Asn Gly Gly Phe Thr Val Pro Phe Tyr Lys Gln Leu Leu Gly Lys Pro
 485 490 495
 Ile Gln Leu Ser Asp Leu Glu Ser Val Asp Pro Glu Leu His Lys Ser
 500 505 510
 Leu Val Trp Ile Leu Glu Asn Asp Ile Thr Ser Val Leu Asp His Thr
 515 520 525
 Phe Cys Val Glu His Asn Ala Phe Gly Arg Leu Leu Gln His Glu Leu
 530 535 540
 Lys Pro Asn Gly Lys Asn Leu Gln Val Thr Glu Glu Asn Lys Lys Glu
 545 550 555 560
 Tyr Val Arg Leu Tyr Val Asn Trp Arg Phe Met Arg Gly Ile Glu Ala
 565 570 575
 Gln Phe Leu Ala Leu Gln Lys Gly Phe Asn Glu Leu Ile Pro Gln His
 580 585 590
 Leu Leu Lys Pro Phe Glu Gln Lys Glu Leu Glu Leu Ile Ile Gly Gly
 595 600 605
 Leu Asp Lys Ile Asp Ile Ser Asp Trp Lys Ala Asn Thr Arg Leu Lys
 610 615 620
 His Cys Leu Ala Asn Ser Asn Ile Val Gln Trp Phe Trp Gln Ala Val
 625 630 635 640
 Glu Ser Phe Asp Glu Glu Arg Arg Ala Arg Leu Leu Gln Phe Val Thr
 645 650 655
 Gly Ser Thr Arg Val Pro Leu Gln Gly Phe Lys Ala Leu Gln Gly Ser
 660 665 670

Thr Gly Ala Ala Gly Pro Arg Leu Phe Thr Ile His Leu Ile Asp Ala
 675 680 685
 Asn Thr Asp Asn Leu Pro Lys Ala His Thr Cys Phe Asn Arg Ile Asp
 690 695 700
 Ile Pro Pro Tyr Glu Ser Tyr Glu Lys Leu Tyr Glu Lys Leu Leu Thr
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 Ala Val Glu Glu Thr Ser Gly Phe Ala Val Glu
 725 730
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 Ala Asp Gly Leu Tyr Lys Arg Asp Val Phe Arg Phe Pro Asp Pro Phe
 20 25 30
 Ala Val Leu Thr Val Asp Gly Glu Gln Thr His Thr Thr Thr Ala Ile
 35 40 45
 Lys Lys Thr Leu Asn Pro Tyr Trp Asn Glu Thr Phe Glu Val Asn Val
 50 55 60
 Thr Asp Asn Ser Thr Ile Ala Ile Gln Val Phe Asp Gln Lys Lys Phe
 65 70 75 80
 Lys Lys Lys Gly Gln Gly Phe Leu Gly Val Ile Asn Leu Arg Val Gly
 85 90 95
 Asp Val Leu Asp Leu Ala Ile Gly Gly Asp Glu Met Leu Thr Arg Asp
 100 105 110
 Leu Lys Lys Ser Asn Glu Asn Thr Val Val His Gly Lys Ile Ile Ile
 115 120 125
 Asn Leu Ser Thr Thr Ala Gln Ser Thr Leu Gln Val Pro Ser Ser Ala
 130 135 140
 Ala Ser Gly Ala Arg Thr Gln Arg Thr Ser Ile Thr Asn Asp Pro Gln
 145 150 155 160
 Ser Ser Lys Ser Ser Ser Val Ser Arg Asn Pro Ala Ser Ser Arg Ala
 165 170 175
 Gly Ser Pro Thr Arg Asp Asn Ala Pro Ala Ala Ser Pro Ala Ser Ser
 180 185 190
 Glu Pro Arg Thr Phe Ser Ser Phe Glu Asp Gln Tyr Gly Arg Leu Pro
 195 200 205
 Pro Gly Trp Glu Arg Arg Thr Asp Asn Leu Gly Arg Thr Tyr Tyr Val
 210 215 220
 Asp His Asn Thr Arg Ser Thr Thr Trp Ile Arg Pro Asn Leu Ser Ser
 225 230 235 240

Val Ala Gly Ala Ala Ala Ala Glu Leu His Ser Ser Ala Ser Ser Ala
245 250 255
Asn Val Thr Glu Gly Val Gln Pro Ser Ser Ser Asn Ala Ala Arg Arg
260 265 270
Thr Glu Ala Ser Val Leu Thr Ser Asn Ala Thr Thr Ala Gly Ser Gly
275 280 285
Glu Leu Pro Pro Gly Trp Glu Gln Arg Tyr Thr Pro Glu Gly Arg Pro
290 295 300
Tyr Phe Val Asp His Asn Thr Arg Thr Thr Thr Trp Val Asp Pro Arg
305 310 315 320
Arg Gln Gln Tyr Ile Arg Ser Tyr Gly Gly Pro Asn Asn Ala Thr Ile
325 330 335
Gln Gln Gln Pro Val Ser Gln Leu Gly Pro Leu Pro Ser Gly Trp Glu
340 345 350
Met Arg Leu Thr Asn Thr Ala Arg Val Tyr Phe Val Asp His Asn Thr
355 360 365
Lys Thr Thr Thr Trp Asp Asp Pro Arg Leu Pro Ser Ser Leu Asp Gln
370 375 380
Asn Val Pro Gln Tyr Lys Arg Asp Phe Arg Arg Lys Leu Ile Tyr Phe
385 390 395 400
Leu Ser Gln Pro Ala Leu His Pro Leu Pro Gly Gln Cys His Ile Lys
405 410 415
Val Arg Arg Asn His Ile Phe Glu Asp Ser Tyr Ala Glu Ile Met Arg
420 425 430
Gln Ser Ala Thr Asp Leu Lys Lys Arg Leu Met Ile Lys Phe Asp Gly
435 440 445
Glu Asp Gly Leu Asp Tyr Gly Gly Leu Ser Arg Glu Tyr Phe Phe Leu
450 455 460
Leu Ser His Glu Met Phe Asn Pro Phe Tyr Cys Leu Phe Glu Tyr Ser
465 470 475 480
Ser Val Asp Asn Tyr Thr Leu Gln Ile Asn Pro His Ser Gly Ile Asn
485 490 495
Pro Glu His Leu Asn Tyr Phe Lys Phe Ile Gly Arg Val Ile Gly Leu
500 505 510
Ala Ile Phe His Arg Arg Phe Val Asp Ala Phe Phe Val Val Ser Phe
515 520 525
Tyr Lys Met Ile Leu Gln Lys Lys Val Thr Leu Gln Asp Met Glu Ser
530 535 540
Met Asp Ala Glu Tyr Tyr Arg Ser Leu Val Trp Ile Leu Asp Asn Asp
545 550 555 560
Ile Thr Gly Val Leu Asp Leu Thr Phe Ser Val Glu Asp Asn Cys Phe
565 570 575

Gly Glu Val Val Thr Ile Asp Leu Lys Pro Asn Gly Arg Asn Ile Glu
 580 585 590
 Val Thr Glu Glu Asn Lys Arg Glu Tyr Val Asp Leu Val Thr Val Trp
 595 600 605
 Ile Gln Lys Arg Ile Glu Glu Gln Phe Asn Ala Phe His Glu Gly Phe
 610 615 620
 Ser Glu Leu Ile Pro Gln Glu Leu Ile Asn Val Phe Asp Glu Arg Glu
 625 630 635 640
 Leu Glu Leu Leu Ile Gly Gly Ile Ser Glu Ile Asp Met Glu Asp Trp
 645 650 655
 Lys Lys His Lys Asp Tyr Arg Ser Tyr Ser Glu Asn Asp Gln Ile Ile
 660 665 670
 Lys Trp Phe Trp Glu Leu Met Asp Glu Trp Ser Asn Glu Lys Lys Ser
 675 680 685
 Arg Leu Leu Gln Phe Thr Thr Gly Thr Ser Arg Ile Pro Val Asn Gly
 690 695 700
 Phe Lys Asp Leu Gln Gly Ser Asp Gly Pro Arg Lys Phe Thr Ile Glu
 705 710 715 720
 Lys Ala Gly Glu Pro Asn Lys Leu Pro Lys Ala His Thr Cys Phe Asn
 725 730 735
 Arg Leu Asp Leu Pro Pro Tyr Thr Ser Lys Lys Asp Leu Asp His Lys
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 Leu Ser Ile Ala Val Glu Glu Thr Ile Gly Phe Gly Gln Glu
 755 760 765

<210> 9
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 <213> Artificial

<220>
 <223> Description of Artificial Sequence: Consensus

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<210> 10
 <211> 11
 <212> PRT
 <213> Artificial

<220>
 <223> Description of Artificial Sequence: Consensus

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 1 5 10

<210> 11
 <211> 6

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<213>  Artificial

<220>
<223>  Description of Artificial Sequence: Consensus

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1              5

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<211>  4
<212>  PRT
<213>  Artificial

<220>
<223>  Description of Artificial Sequence: Consensus

<220>
<221>  misc_feature
<222>  3
<223>  Xaa = Any amino acid

<400>  12
Pro Pro Xaa Tyr
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<210>  13
<211>  5
<212>  PRT
<213>  Artificial

<220>
<223>  Description of Artificial Sequence: Consensus

<400>  13
Pro Pro Pro Pro Tyr
1              5

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